



TCCGCAGGCGGACCGGGGGCAAAGGAGGTGGCATGTCCGGTCAGGCACAGCAGGGTCCTGT  
 GTCCGCGCTGAGCCGCGCTCTCCCTGTCCAGCAAGGACC  
 ><Met {trans=1-s, dir=f, res=1}>  
 ATGAGGGCGCTGGAGGGGCCAGGCCTGTGCTGTGCCTGGTGTGGCGCTGCCTGCC  
 CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC  
 GCAGAGACAGGGGAGCGGCTGGTGTGCGCCCACTGCCCCCAGGCACCTTTGTGCAGCGG  
 CCGTGCCGCGGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG  
 TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG  
 GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCTGCCGCTGCCGCACCGGCTTCTTC  
 GCGCACGCTGGTTTCTGCTTGAGCAGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC  
 CCGGGCACCCCAAGCAGAACACGAGTGCCAGCCGTGCCCCCAAGGCACCTTCTCAGCC  
 AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACCGCCCTGGGCCTGGCC  
 CTCATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAGCTGCACTGGCTTCCCC  
 CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT  
 TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCGGAG  
 GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCTTGCAGCTGAAGCTGCGTCGGCGG  
 CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTG  
 CGCGTGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC  
 TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCACTTGCACTGAAAGAGG  
 CTTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

Fig. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
CAGTTCTGGAANTAAGTGGAGCNCTGCCGCTACTGNAACGTCTCTGNNG  
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT  
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC  
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA  
GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT  
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG  
CGTGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCAT

Fig. 3

SEQ ID NO: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
 SEQ ID NO: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
 SEQ ID NO: 6 1  
 SEQ ID NO: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
 G  
 SEQ ID NO: 4 178 CA-TTCTGGAACCTACCTGGAGCGC  
 SEQ ID NO: 5 51 CAGTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG  
 SEQ ID NO: 6 2 CAGTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG  
 SEQ ID NO: 3 51 CAGTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG  
 SEQ ID NO: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCCGCGCT  
 SEQ ID NO: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCCGTCCT  
 SEQ ID NO: 7 1 GAGGGCCCCCAGGAGTGGTGGCCGGAGGTG  
 SEQ ID NO: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCCGTCCT  
 SEQ ID NO: 5 151 GCNGCTGCAGCACCCGGNTTCTTCGCGCACGCTGNTTCTGCTTGGAGCAC  
 SEQ ID NO: 6 102 GCCGCTGCCGCACCCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC  
 SEQ ID NO: 7 32 TGGCAGGGGTACAGTTGCTGTGTCGCCAGCCTTGACCCCTGAGCTAGGACAC  
 SEQ ID NO: 3 151 GCCGCTGCCGCACCCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC  
 SEQ ID NO: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA  
 SEQ ID NO: 6 152 GCATCGTGTCCACCTGGTGCCTGGCGTGATTNCCCGGCGACCCCCAGCCA  
 SEQ ID NO: 7 82 CAGTTCCCTGACCTGTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA  
 SEQ ID NO: 8 1 GCATCGTGTCCACCTGGTGCCTGGCGTGATTGCCCGGCGACCCCCAGCCA  
 SEQ ID NO: 10 1 CTTGTCCACCTGGTGCCTGGCGTGATTNCCC-GGGCACCCCCAGCCA  
 SEQ ID NO: 3 201 GCATCGTGTCCACCTGGTGCCTGGCGTGATTGCCCGGCGACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA - TGCAAAAGCCGTG  
 SEQ ID NO: 7 132 GAACACGCAGN - CC - AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 8 51 GAACACGCAG - GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 10 47 GAACACGCAGTGCC - AGCCNT - CCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 9 1 AGCNGTGCCNCCNAGGCACCTTCTCAGCCAGCAGT  
 SEQ ID NO: 3 251 GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT  
 SEQ ID NO: 8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT  
 SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGNC - T  
 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT  
 SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT  
 SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAG  
 SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAGCT  
 SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAGCT  
 SEQ ID NO: 9 86 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAGCT  
 SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAGCT  
 SEQ ID NO: 10 197 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG  
 SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG  
 SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG  
 SEQ ID NO: 10 247 CGTGCCGTGATCGACTTTGTGGCTTTCAGGACATCTCCAT  
 SEQ ID NO: 9 186 CGTGCCGTGATCGACTTTGTGGCTTTCAGGACATCTCCAT  
 SEQ ID NO: 3 451 CGTGCCGTGATCGACTTTGTGGCTTTCAGGACATCTCCAT

Fig. 4 (cont.)

DNA 30942  
H1NFR2

1 MRALECGFGLSLLCEVIALPALLPVPAVHGVAIIPITYPWFD AEIG  
1 MAPVAVWALAVGLLWAAAHALPAQVAFIPY APLDGSICRLREYDQI

DNA 30942  
H1NFR2

CRD1 CRD2

45 ERLVCAQCPRPGTFVQRPCCRDSPTTCGP C PPRHYIQFWHYLERCRYCHVL  
50 AOMCCKSKCSPGQNAKVFCXTXISDITVCDSCGEOSTYTQLWNWVPECISCGSR

DNA 30942  
H1NFR2

CRD2 CRD3

75 CGEREEEARACHATHMRAICRCRTGFF...AKAG...FLEHASCPPGAGV  
100 CSSDQVETOACTREONRICTCRPGWYCALSKEGCRLCAPLRKCRPGFGV

DNA 30942  
H1NFR2

CRD3 CRD4

129 IAPGTFSQNTQCPCPPGTFSASSSSSEQCOPHRHCTALGLALMVPGSSS  
150 ARPGETETSDVCKPCAPGTFSNTTSSSTDICRPHQICHVVA...IPGNAS

DNA 30942  
H1NFR2

CRD4

189 HDTLCTSGTGFP LSTRYPGAECEERAVIDFVAFODISIKRLORLLOALEA  
196 RDAVCTSTST...PTRSMAPGAVHLPQPVSTRSNTQPTPEPSTAPSTSFLL

DNA 30942  
H1NFR2

229 PEGWGPTP...RAGRAALQLKLRRRLTELLGAQDGALLVRLLOALRVARMP  
244 PMGPPSPAEGSTGDFALPYGLIVGVITALGLLLIGVVHCVIMTQVKKKPL

DNA 30942  
H1NFR2

287 GLERSYRERFLPVH  
293 CLQREAKVPHLPADKARGTQGPEQOHLLITAPSSSSSSLESSASALORRA

H1NFR2

343 PTRNOPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSO

H1NFR2

393 HSSQCSSQASSTMGDTDSSSPSES PKOEQVPFSKEECAFRSOLETPETLLG

H1NFR2

443 STEEKPLPLGVDPDAGMKPS

Fig. 5

DcR3 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A 31  
 OPG 1 M N K L L C C A L V F L D I S I K W T T Q E T F P . . . . . 25

CRD1  
 DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62  
 OPG 26 - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93  
 OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD2  
 DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124  
 OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3  
 DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155  
 OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD4  
 DcR3 156 G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S 186  
 OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217  
 OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247  
 OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277  
 OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300  
 OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

Fig. 6

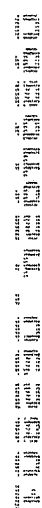


Fig. 7



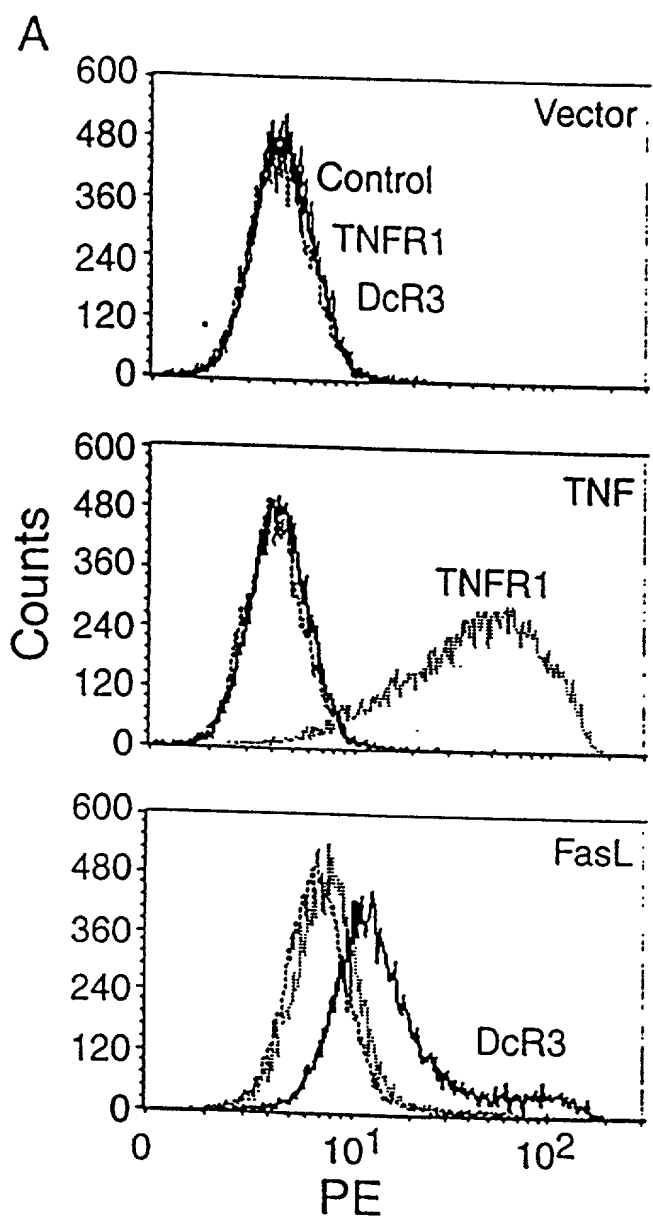
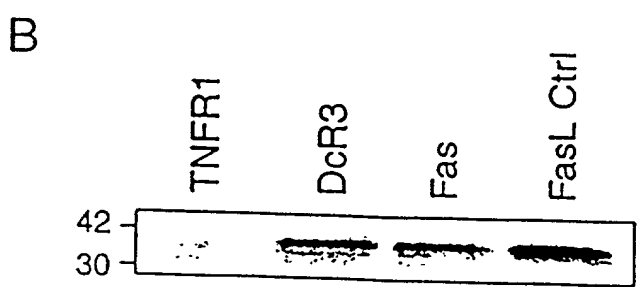


Fig. 8



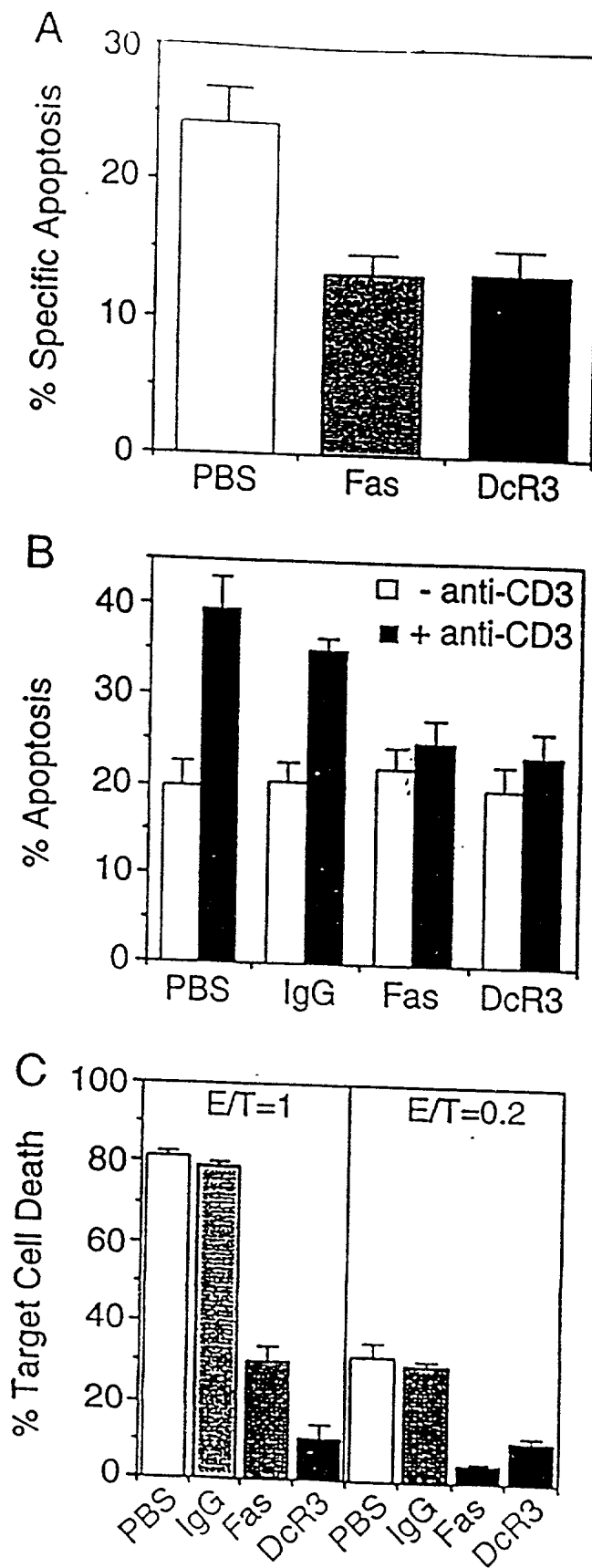


Fig. 9

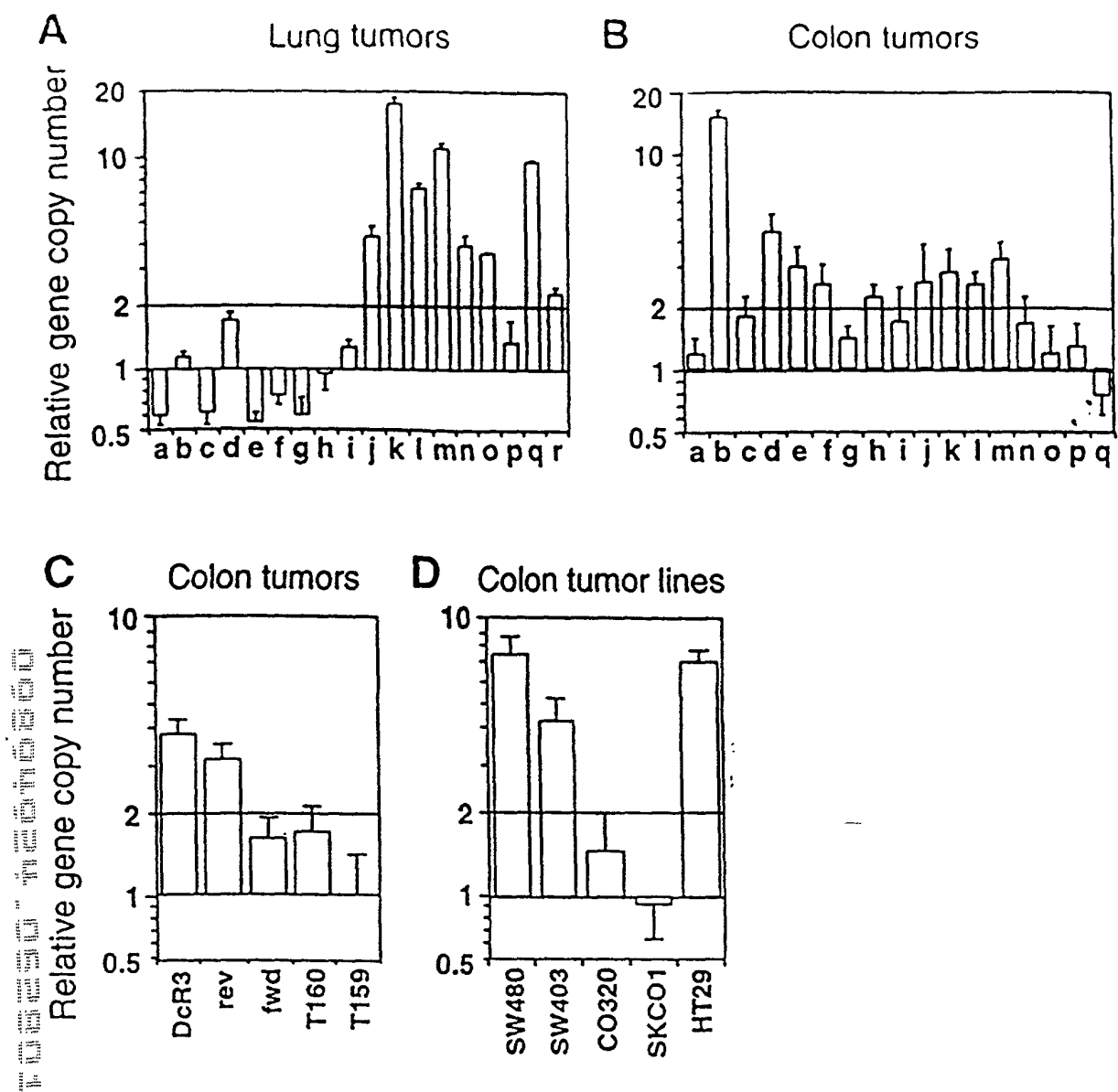


Fig. 10

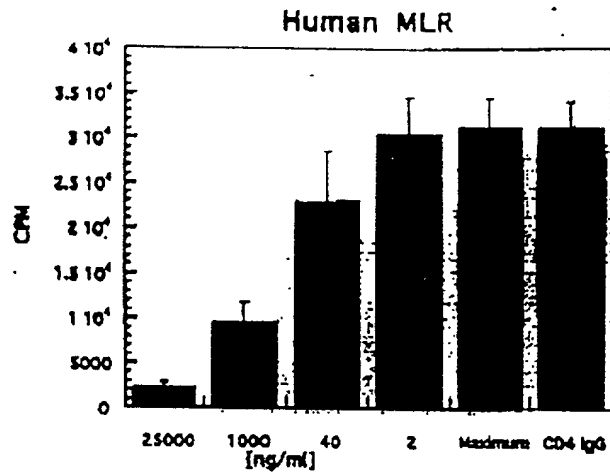


Fig. 11A

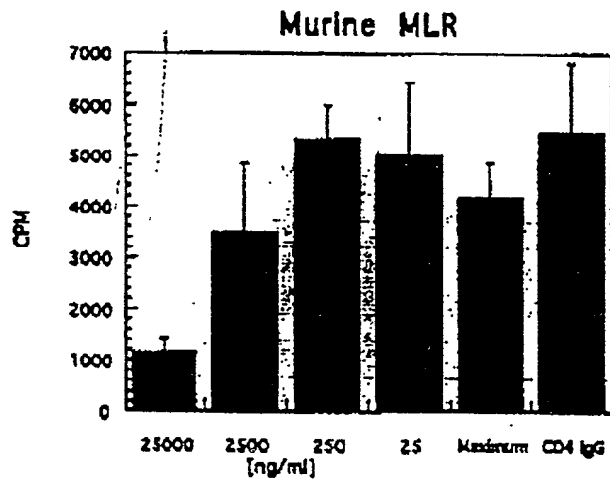


Fig. 11B

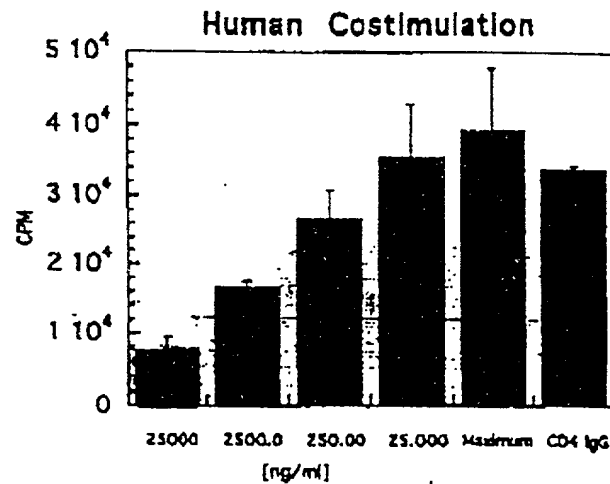


Fig. 11C

|   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 2 | 2 | 1 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 3 | 3 | 2 | 1 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 4 | 4 | 3 | 2 | 1 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 5 | 5 | 4 | 3 | 2 | 1 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |

Antigen specificity was determined using 10 microgram/ml mAb.  
 \* blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

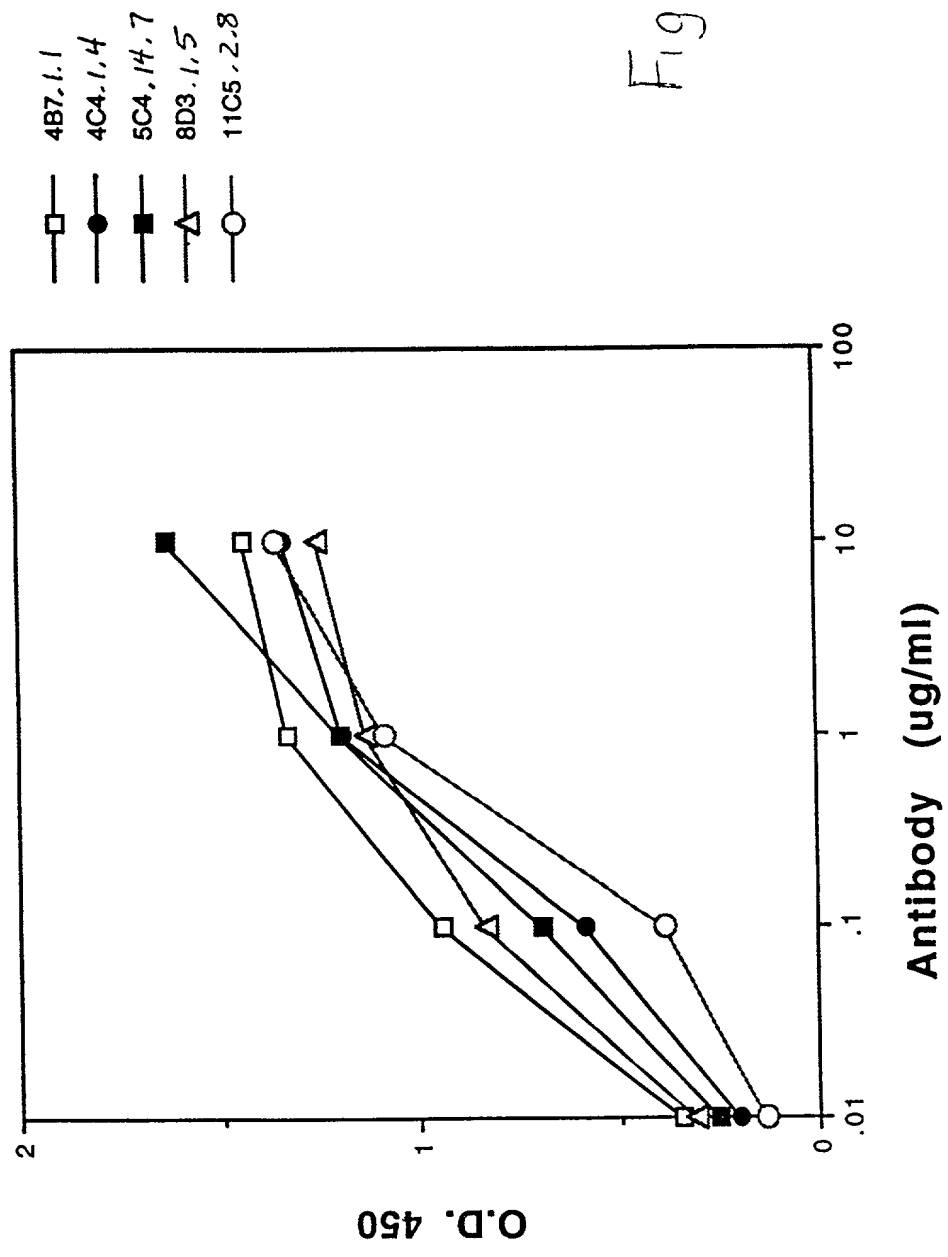


Fig. 13

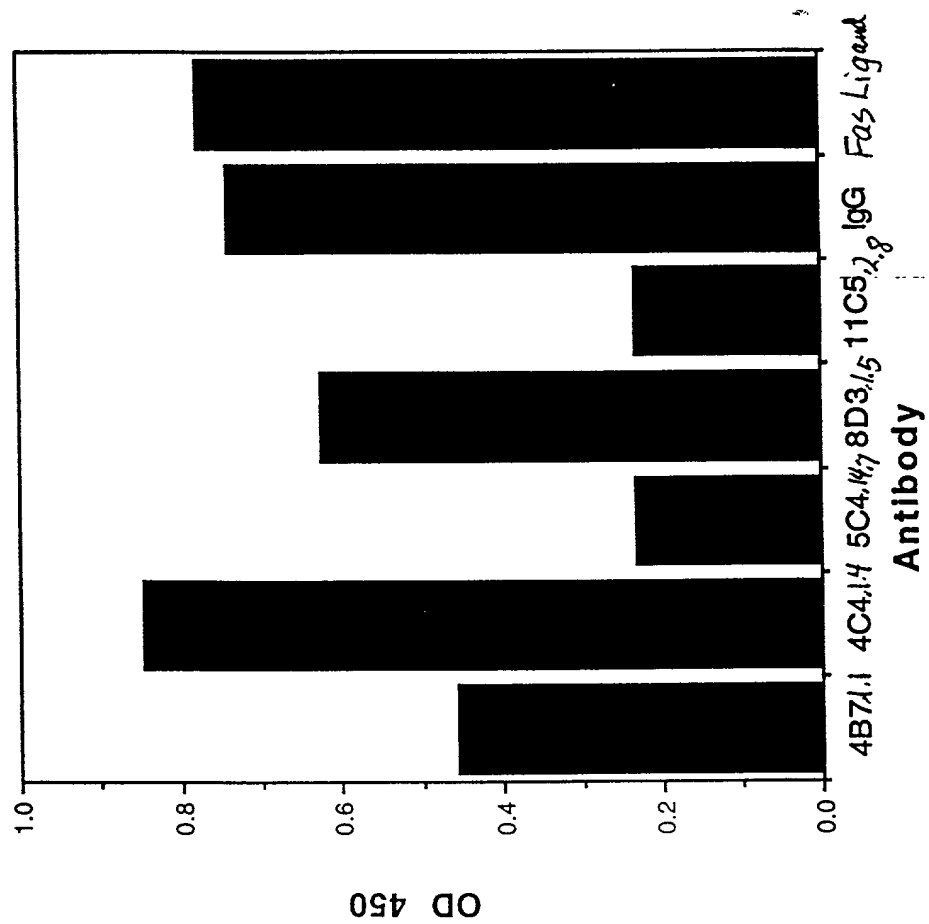


Fig. 14